

\$%^STN;HighlightOn= ***;HighlightOff=*** ;
=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 11:25:54 ON 08 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA Lexicon is the copyrighted intellectual property of the the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS, is strictly prohibited.

FILE COVERS 1907 - 8 Feb 2005 VOL 142 ISS 7
FILE LAST UPDATED: 7 Feb 2005 (20050207/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=>
=>

=> d stat que
L1 100 SEA FILE=REGISTRY ABB=ON PLU=ON EEMQRR/SQSP
L2 5 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<=50
L4 6 SEA FILE=HCAPLUS ABB=ON PLU=ON L2

=> => d ibib abs hitrn l4 1-6

L4 ANSWER 1 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:993109 HCAPLUS
DOCUMENT NUMBER: 141:415634
TITLE: Skin compositions containing anti-aging peptides and polyhydric alcohols
INVENTOR(S): Hirano, Nobuyuki; Adachi, Katsuyoshi; Tada, Takahiro; Ito, Shiho; Aramaki, Kaname
PATENT ASSIGNEE(S): Mikimoto Pharmaceutical Co., Ltd., Japan; Toshin Kagaku Co., Ltd.
SOURCE: Jpn. Kokai Tokkyo Koho, 11 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	----	-----	-----	-----
JP 2004323401	A2	20041118	JP 2003-118442	20030423
PRIORITY APPLN. INFO.:			JP 2003-118442	20030423
AB	The invention relates to a skin compn. contg. Glu-Glu-Met-Gln-Arg-Arg			

peptide and polyhydric alc. having .gtoreq. 2 OH groups, wherein the compn. shows improved effect of the peptide. Skin compns. contg. the hexapeptide, polyhydric alcs., and other active components are also disclosed. A cosmetic lotion contg. Glu-Glu-Met-Gln-Arg-Arg peptide soln. (Argireline soln.) 10, glycerin 10, Me paraben 0.2, and water balance to 100 % was formulated.

IT ***304432-12-0*** , Argireline
RL: COS (Cosmetic use); BIOL (Biological study); USES (Uses)
(skin compns. contg. anti-aging peptides and polyhydric alcs. with other defined active components)

L4 ANSWER 2 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:993108 HCAPLUS
DOCUMENT NUMBER: 141:415633
TITLE: Skin compositions containing anti-aging peptides and other active comonents
INVENTOR(S): Adachi, Katsuyoshi; Tada, Takahiro; Ito, Shiho; Aramaki, Kaname
PATENT ASSIGNEE(S): Mikimoto Pharmaceutical Co., Ltd., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 24 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2004323400	A2	20041118	JP 2003-118441	20030423
PRIORITY APPLN. INFO.:			JP 2003-118441	20030423

AB The invention relates to a skin compn. characterized by contg. (1) Glu-Glu-Met-Gln-Arg-Arg peptide, and (2) skin moisturizer, cell activator, antiinflammatory agent, antioxidant, skin-whitening agent, hyaluronidase inhibitor, anti-plasmin agent, active oxygen inhibitor, collagenase inhibitor, and/or antihistamine, wherein the combination of the peptide and other active components improves the effect. A compn. contg. Glu-Glu-Met-Gln-Arg-Arg peptide soln. (Argireline soln.) 10, glycerin 5, Me paraben 0.2, Evolvulus alsinoides ext. 2, and water balance to 100 % was formulated.

IT ***304432-12-0*** , Argireline
RL: COS (Cosmetic use); BIOL (Biological study); USES (Uses)
(skin compns. contg. anti-aging peptides and other active comonents)

L4 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:390948 HCAPLUS
DOCUMENT NUMBER: 140:428678
TITLE: Use of a synergistic combination of calcium-channel antagonists for preventing or treating wrinkles
INVENTOR(S): Renault, Beatrice
PATENT ASSIGNEE(S): L'Oreal, Fr.
SOURCE: Fr. Demande, 23 pp.
CODEN: FRXXBL
DOCUMENT TYPE: Patent
LANGUAGE: French
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
FR 2846885	A1	20040514	FR 2002-14183	20021113
FR 2846885	B1	20041224		
EP 1419764	A1	20040519	EP 2003-292767	20031105
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
JP 2004161773	A2	20040610	JP 2003-383084	20031112
US 2004147443	A1	20040729	US 2003-705857	20031113
PRIORITY APPLN. INFO.:			FR 2002-14183	A 20021113
			US 2002-427575P	P 20021120

AB The invention relates to a compn. adapted to topical application on the skin, including, in a physiol. acceptable medium, (i) at least a peptide or a mixt. of peptides including a sequence of amino acids derived from the sequence of amino acids of the protein SNAP 25 and (ii) at least one inhibitor of calcium channels. Also intended is a compn. adapted to a topical application on the skin, as an agent to prevent or treat the wrinkles and fine lines, in particular the wrinkles of expression, as well as a process of cosmetic treatment including the application on the skin of the aforementioned compn.

IT ***304432-12-0*** ***304432-13-1***

RL: BSU (Biological study, unclassified); COS (Cosmetic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (amino acid sequence; synergistic combination of calcium-channel antagonists for preventing or treating wrinkles)

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:40900 HCAPLUS

DOCUMENT NUMBER: 140:229634

TITLE: Small peptides patterned after the N-terminus domain of SNAP25 inhibit SNARE complex assembly and regulated exocytosis

AUTHOR(S): Blanes-Mira, Clara; Merino, Jaime M.; Valera, Elvira; Fernandez-Ballester, Gregorio; Gutierrez, Luis M.; Viniegra, Salvador; Perez-Paya, Enrique; Ferrer-Montiel, Antonio

CORPORATE SOURCE: Instituto de Biologia Molecular y Celular, Universidad Miguel Hernandez, Alicante, Spain

SOURCE: Journal of Neurochemistry (2004), 88(1), 124-135
CODEN: JONRA9; ISSN: 0022-3042

PUBLISHER: Blackwell Publishing Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Synthetic peptides patterned after the C-terminus of synaptosomal assocd. protein of 25 kDa (SNAP25) efficiently abrogate regulated exocytosis. In contrast, the use of SNAP25 N-terminal-derived peptides to modulate SNAP receptors (SNARE) complex assembly and neurosecretion has not been explored. The N-terminus of SNAP25, specially the segment that encompasses 22Ala-44Ile, is essential for the formation of the SNARE complex. Peptides patterned after this protein domain are potent inhibitors of SNARE complex formation. The inhibitory activity correlated with their propensity to adopt an .alpha.-helical secondary structure. These peptides abrogated SNARE complex formation only when added previous to the onset of aggregate assembly. Anal. of the mechanism of action revealed that these peptides disrupted the binary complex formed by SNAP25

and syntaxin. The identified peptides inhibited Ca²⁺-dependent exocytosis from detergent-permeabilized excitable cells. Noteworthy, these amino acid sequences markedly protected intact hippocampal neurons against hypoglycemia-induced, glutamate-mediated excitotoxicity with a potency that rivaled that displayed by botulinum neurotoxins. The authors' findings indicate that peptides patterned after the N-terminus of SNAP25 are potent inhibitors of SNARE complex formation and neuronal exocytosis. Because of their activity in intact neurons, these cell permeable peptides may be hits for antispasmodic and analgesic drug development.

IT ***668487-37-4*** ***668487-39-6***

RL: BSU (Biological study, unclassified); PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(small peptides patterned after N-terminus domain of SNAP25 inhibit SNARE complex assembly and regulated exocytosis in relation to neuroprotection in cultured murine hippocampal neurons)

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:220680 HCAPLUS

DOCUMENT NUMBER: 139:341423

TITLE: Antiaging synthetic hexapeptides

AUTHOR(S): Passerini, Elena

CORPORATE SOURCE: R & D, Lipotec SA, Barcelona, Spain

SOURCE: Cosmetic Technology (Milano, Italy) (2002), 5(6), 37-39

CODEN: CTECFI; ISSN: 1127-6312

PUBLISHER: C.E.C. sas

DOCUMENT TYPE: Journal

LANGUAGE: Italian

AB Some peptides mimic the anti-wrinkle effects of Botox (botulinum neurotoxin type A). The hexapeptide Ac-EEMQRR-NH₂ (part of the N-terminal region of SNAP-25) can inhibit the Ca-dependent release of catecholamines from chromaffin cells and is of value for antiaging cosmetic application.

IT ***616204-22-9***

RL: COS (Cosmetic use); PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antiaging synthetic hexapeptides)

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 6 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:772663 HCAPLUS

DOCUMENT NUMBER: 133:340249

TITLE: Neuronal exocytosis-inhibiting peptides and cosmetic and pharmaceutical compositions containing them

INVENTOR(S): Blanes Mira, Ma. Clara; Llobregat Hernandez, Ma. Mercedes; Gil Tebar, Ana Isabel; Fernandez Ballester, Gregorio Joaquin; Planell Cases, Rosa Ma.; Ferrer Montiel, Antonio Vicente; Viniegra Bover, Salvador; Gutierrez Perez, Luis Miguel; Carbonell Castell, Teresa; Perez Paya, Enrique

PATENT ASSIGNEE(S): Lipotec, S.A., Spain

SOURCE: PCT Int. Appl., 40 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: Spanish
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000064932	A1	20001102	WO 2000-ES58	20000218
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
ES 2160485	A1	20011101	ES 1999-844	19990423
ES 2160485	B1	20020516		
CA 2370289	AA	20001102	CA 2000-2370289	20000218
BR 2000011152	A	20020219	BR 2000-11152	20000218
EP 1180524	A1	20020220	EP 2000-905076	20000218
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002542777	T2	20021217	JP 2000-614281	20000218
PRIORITY APPLN. INFO.:			ES 1999-844	A 19990423
			WO 2000-ES58	W 20000218
AB	The peptide has a sequence of 3 to 30 adjacent amino acids from the amino end of protein SNAP-25 and is useful as neuronal exocytosis inhibitor. The cosmetic and pharmaceutical compns. contain said peptide and optionally one or more peptides from the carboxyl end of SNAP-25. Said compns. are suitable for the treatment of facial wrinkles and asymmetry and pathol. neuronal exocytosis-mediated disorders and alterations.			
IT	***304432-12-0P*** ***304432-13-1P***			
RL: BUU (Biological use, unclassified); PNU (Preparation, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)				
(neuronal exocytosis-inhibiting peptides and cosmetic and pharmaceutical compns. contg. them)				
REFERENCE COUNT:	3	THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT		

=> fil reg

FILE 'REGISTRY' ENTERED AT 11:26:55 ON 08 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 7 FEB 2005 HIGHEST RN 827299-31-0
DICTIONARY FILE UPDATES: 7 FEB 2005 HIGHEST RN 827299-31-0

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

Please note that search-term pricing does apply when

conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=>
=>

=> => fil reg
FILE 'REGISTRY' ENTERED AT 11:34:10 ON 08 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 7 FEB 2005 HIGHEST RN 827299-31-0
DICTIONARY FILE UPDATES: 7 FEB 2005 HIGHEST RN 827299-31-0

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=>
=>

=> d l2 .seq 1-5

L2 ANSWER 1 OF 5 REGISTRY COPYRIGHT 2005 ACS on STN
RN 668487-39-6 REGISTRY
CN L-Alaninamide, N-acetyl-L-.alpha.-glutamyl-L-leucyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-methionyl-L-glutamyl-L-arginyl-L-arginyl-L-alanyl-L-.alpha.-aspartyl-L-glutamyl-L-leucyl- (9CI) (CA INDEX NAME)
NTE modified

type	-----	location	-----	description
terminal mod.	Glu-1	-		N-acetyl
terminal mod.	Ala-13	-		C-terminal amide

SQL ***13***
SQL ***13***

SEQ 1 ELEEMQRRAD QLA

=====

HITS AT: 3-8

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 140:229634

L2 ANSWER 2 OF 5 REGISTRY COPYRIGHT 2005 ACS on STN
RN 668487-37-4 REGISTRY
CN L-Leucinamide, N-acetyl-L-methionyl-L-alanyl-L-.alpha.-glutamyl-L-.alpha.-
aspartyl-L-alanyl-L-.alpha.-aspartyl-L-methionyl-L-arginyl-L-asparaginyl-L-
.alpha.-glutamyl-L-leucyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-
methionyl-L-glutamyl-L-arginyl-L-arginyl-L-alanyl-L-.alpha.-aspartyl-L-
glutamyl- (9CI) (CA INDEX NAME)
NTE modified

type	location		description
terminal mod.	Met-1	-	N-acetyl
terminal mod.	Leu-21	-	C-terminal amide

SQL ***21***
SQL ***21***

SEQ 1 MAEDADMRNE LEEMQRRADQ L

=====

HITS AT: 12-17

REFERENCE 1: 140:229634

L2 ANSWER 3 OF 5 REGISTRY COPYRIGHT 2005 ACS on STN
RN 616204-22-9 REGISTRY
CN L-Argininamide, N-acetyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-methionyl-
L-glutamyl-L-arginyl- (9CI) (CA INDEX NAME)
NTE modified

type	location		description
terminal mod.	Glu-1	-	N-acetyl
terminal mod.	Arg-6	-	C-terminal amide

SQL ***6***
SQL ***6***

SEQ 1 EEMQRR

=====

HITS AT: 1-6

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:341423

L2 ANSWER 4 OF 5 REGISTRY COPYRIGHT 2005 ACS on STN
RN 304432-13-1 REGISTRY
CN L-Alanine, L-.alpha.-glutamyl-L-leucyl-L-.alpha.-glutamyl-L-.alpha.-
glutamyl-L-methionyl-L-glutamyl-L-arginyl-L-arginyl-L-alanyl-L-.alpha.-
aspartyl-L-glutamyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 4: PN: FR2846885 SEQID: 3 claimed sequence

CN 4: PN: WO0064932 SEQID: 3 claimed sequence

SQL ***13***

SQL ***13***

SEQ 1 ELEEMQRRAD QLA

=====

HITS AT: 3-8

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 140:428678

REFERENCE 2: 133:340249

L2 ANSWER 5 OF 5 REGISTRY COPYRIGHT 2005 ACS on STN

RN 304432-12-0 REGISTRY

CN L-Arginine, L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-methionyl-L-glutaminyl-L-arginyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2: PN: FR2846885 SEQID: 2 claimed sequence

CN 3: PN: WO0064932 SEQID: 2 claimed sequence

CN Argireline

SQL ***6***

SQL ***6***

SEQ 1 EEMQRR

=====

HITS AT: 1-6

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 141:415634

REFERENCE 2: 141:415633

REFERENCE 3: 140:428678

REFERENCE 4: 133:340249

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 11:34:37 ON 08 FEB 2005

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA Lexicon is the copyrighted intellectual property of the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS, is

strictly prohibited.

FILE COVERS 1907 - 8 Feb 2005 VOL 142 ISS 7

FILE LAST UPDATED: 7 Feb 2005 (20050207/ED)

This file contains CAS Registry Numbers for easy and accurate
substance identification.

=>

=>

=>

=> d stat que

L1 100 SEA FILE=REGISTRY ABB=ON PLU=ON EEMQRR/SQSP
L2 5 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<=50
L3 95 SEA FILE=REGISTRY ABB=ON PLU=ON L1 NOT L2
L4 6 SEA FILE=HCAPLUS ABB=ON PLU=ON L2
L5 49 SEA FILE=HCAPLUS ABB=ON PLU=ON L3
L6 47 SEA FILE=HCAPLUS ABB=ON PLU=ON L5 NOT L4
L7 25 SEA FILE=HCAPLUS ABB=ON PLU=ON L6 AND PATENT/DT
L8 17 SEA FILE=HCAPLUS ABB=ON PLU=ON L7 AND PD=<NOVEMBER 13, 2003
L9 22 SEA FILE=HCAPLUS ABB=ON PLU=ON L6 NOT L7
L10 11 SEA FILE=HCAPLUS ABB=ON PLU=ON L9 NOT (2005 OR 2004)/PY
L11 28 SEA FILE=HCAPLUS ABB=ON PLU=ON L8 OR L10

=> d ibib abs hitstr l11 1-28

L11 ANSWER 1 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:766692 HCAPLUS

TITLE: cDNA and protein sequences of human
synaptosomal-associated membrane protein-25 their
therapeutic uses for amnesia

INVENTOR(S): Jing, Naihe; Li, Baoming; Jin, Meilai; Gao, Xiang;
Hou, Qiuling; Tu, Yanyang; Wang, Xinming

PATENT ASSIGNEE(S): Shanghai Institute of Biochemistry, Chinese Academy of
Sciences, Peop. Rep. China; Shanghai Institute of
Physiology, Chinese Academy of Sciences; Shanghai
Bioengineering Research Center, Chinese Academy of
Sciences; Fudan University

SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 35 pp.
CODEN: CNXXEV

DOCUMENT TYPE: ***Patent***

LANGUAGE: Chinese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CN 1408881	A	20030409	CN 2001-126749	20010914 <--
PRIORITY APPLN. INFO.:			CN 2001-126749	20010914

AB This invention provides cDNA and protein sequences of human
synaptosomal-assocd. membrane protein-25 (SNAP-25). The expression level
of both SNAP-25 gene and protein was increased in the training rat.
Introducing antisense SNAP-25 gene into rat hippocampus CA1 and CA3 region
resulted in the disruption of long term potentiation and reducing the
learning and memory ability of rat. The SNAP-25 provided in this
invention can be used for diagnosis, treatment and drug screening of
amnesia.

IT ***825667-86-5***

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP
(Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; cDNA and protein sequences of human
synaptosomal-assocd. membrane protein-25 their therapeutic uses for
amnesia)

RN 825667-86-5 HCAPLUS

CN INDEX NAME NOT YET ASSIGNED

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 2 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:875393 HCAPLUS

DOCUMENT NUMBER: 139:363045

TITLE: Genes expressed in atherosclerotic tissue and their use in diagnosis and pharmacogenetics

INVENTOR(S): Nevins, Joseph; West, Mike; Goldschmidt, Pascal

PATENT ASSIGNEE(S): Duke University, USA

SOURCE: PCT Int. Appl., 408 pp.

CODEN: PIXXD2

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003091391	A2	20031106	WO 2002-US38221	20021112 <--
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2003091391	A2	20031106	WO 2002-XA38221	20021112 <--
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2003091391	A2	20031106	WO 2002-XB38221	20021112 <--
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003224383	A1	20031204	US 2002-291885	20021112
PRIORITY APPLN. INFO.:			US 2002-374547P	P 20020423
			US 2002-420784P	P 20021024
			US 2002-421043P	P 20021025
			US 2002-424680P	P 20021108
			WO 2002-US38221	A 20021112

AB Genes whose expression is correlated with an determinant of an atherosclerotic phenotype are provided. Also provided are methods of using the subject atherosclerotic determinant genes in diagnosis and treatment methods, as well as drug screening methods. In addn., reagents and kits thereof that find use in practicing the subject methods are provided. Also provided are methods of detg. whether a gene is correlated with a disease phenotype, where correlation is detd. using a Bayesian anal.

IT ***459518-10-6*** , GenBank BAA22370
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genes expressed in atherosclerotic tissue and their use in diagnosis and pharmacogenetics)
RN 459518-10-6 HCAPLUS
CN GenBank BAA22370 (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 3 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:765153 HCAPLUS

DOCUMENT NUMBER: 139:241383

TITLE: Expressed sequence tags from cDNA libraries derived from human mRNAs having intact 5' ends and their encoded secreted proteins

INVENTOR(S): Tanaka, Hiroaki; Dumas Milne, Edwards Jean-Baptiste; Giordano, Jean-Yves; Jobert, Severin; Bejanin, Stephane

PATENT ASSIGNEE(S): Genset, Fr.

SOURCE: Can. Pat. Appl., 163 pp.

CODEN: CPXXEB

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 13

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CA 2343602	AA	20011018	CA 2001-2343602	20010417 <--
CA 2343602	AA	20011018	CA 2001-2343602	20010417 <--
PRIORITY APPLN. INFO.:			US 2000-197873P	P 20000418
			CA 2001-2343602	A 20010417

AB The sequences of 5' ESTs and consensus contigated 5' ESTs derived from cDNA libraries derived from mRNAs having intact 5' ends are disclosed. The 5' ESTs and consensus contigated 5' ESTs may be used to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used to design expression vectors and secretion vectors. [This abstr. record is one of thirteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT ***599431-67-1***

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; expressed sequence tags from cDNA libraries)

derived from human mRNAs having intact 5' ends and their encoded secreted proteins)

RN 599431-67-1 HCAPLUS

CN Protein (human clone CA2343602-SEQID-24942) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 4 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:765151 HCAPLUS

DOCUMENT NUMBER: 139:241382

TITLE: Expressed sequence tags from cDNA libraries derived from human mRNAs having intact 5' ends and their encoded secreted proteins

INVENTOR(S): Tanaka, Hiroaki; Dumas Milne, Edwards Jean-Baptiste; Giordano, Jean-Yves; Jobert, Severin; Bejanin, Stephane

PATENT ASSIGNEE(S): Genset, Fr.

SOURCE: Can. Pat. Appl., 163 pp.

CODEN: CPXXEB

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 13

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CA 2343602	AA	20011018	CA 2001-2343602	20010417 <--
CA 2343602	AA	20011018	CA 2001-2343602	20010417 <--
PRIORITY APPLN. INFO.:			US 2000-197873P	P 20000418
			CA 2001-2343602	A 20010417

AB The sequences of 5' ESTs and consensus contigated 5' ESTs derived from cDNA libraries derived from mRNAs having intact 5' ends are disclosed. The 5' ESTs and consensus contigated 5' ESTs may be used to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used to design expression vectors and secretion vectors. [This abstr. record is one of thirteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT ***599366-06-0*** ***599373-73-6***

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses) (amino acid sequence; expressed sequence tags from cDNA libraries derived from human mRNAs having intact 5' ends and their encoded secreted proteins)

RN 599366-06-0 HCAPLUS

CN Protein (human clone CA2343602-SEQID-20246) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 599373-73-6 HCAPLUS

CN Protein (human clone CA2343602-SEQID-20804) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 5 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:765150 HCAPLUS
DOCUMENT NUMBER: 139:241381
TITLE: Expressed sequence tags from cDNA libraries derived
from human mRNAs having intact 5' ends and their
encoded secreted proteins
INVENTOR(S): Tanaka, Hiroaki; Dumas Milne, Edwards Jean-Baptiste;
Giordano, Jean-Yves; Jobert, Severin; Bejanin,
Stephane
PATENT ASSIGNEE(S): Genset, Fr.
SOURCE: Can. Pat. Appl., 163 pp.
CODEN: CPXXEB
DOCUMENT TYPE: ***Patent***
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 13
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CA 2343602	AA	20011018	CA 2001-2343602	20010417 <--
CA 2343602	AA	20011018	CA 2001-2343602	20010417 <--

PRIORITY APPLN. INFO.:
US 2000-197873P P 20000418
CA 2001-2343602 A 20010417

AB The sequences of 5' ESTs and consensus contigated 5' ESTs derived from
cDNA libraries derived from mRNAs having intact 5' ends are disclosed.
The 5' ESTs and consensus contigated 5' ESTs may be used to obtain cDNAs
and genomic DNAs corresponding to the 5' ESTs and consensus contigated 5'
ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used in
diagnostic, forensic, gene therapy, and chromosome mapping procedures.
Upstream regulatory sequences may also be obtained using the 5' ESTs and
consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5'
ESTs may also be used to design expression vectors and secretion vectors.
[This abstr. record is one of thirteen records for this document
necessitated by the large no. of index entries required to fully index the
document and publication system constraints.].

IT ***599359-78-1*** ***599359-79-2***
RL: BSU (Biological study, unclassified); BUU (Biological use,
unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; expressed sequence tags from cDNA libraries
derived from human mRNAs having intact 5' ends and their encoded
secreted proteins)

RN 599359-78-1 HCAPLUS
CN Protein (human clone CA2343602-SEQID-17001 N-terminal fragment) (9CI) (CA
INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 599359-79-2 HCAPLUS
CN Protein (human clone CA2343602-SEQID-17002 N-terminal fragment) (9CI) (CA
INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 6 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:765147 HCAPLUS
DOCUMENT NUMBER: 139:241380
TITLE: Expressed sequence tags from cDNA libraries derived
from human mRNAs having intact 5' ends and their

INVENTOR(S): encoded secreted proteins
Tanaka, Hiroaki; Dumas Milne, Edwards Jean-Baptiste;
Giordano, Jean-Yves; Jobert, Severin; Bejanin,
Stephane
PATENT ASSIGNEE(S): Genset, Fr.
SOURCE: Can. Pat. Appl., 163 pp.
CODEN: CPXXEB
DOCUMENT TYPE: ***Patent***
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 13
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CA 2343602	AA	20011018	CA 2001-2343602	20010417 <--
CA 2343602	AA	20011018	CA 2001-2343602	20010417 <--
PRIORITY APPLN. INFO.:			US 2000-197873P	P 20000418
			CA 2001-2343602	A 20010417

AB The sequences of 5' ESTs and consensus contigated 5' ESTs derived from cDNA libraries derived from mRNAs having intact 5' ends are disclosed. The 5' ESTs and consensus contigated 5' ESTs may be used to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used to design expression vectors and secretion vectors. [This abstr. record is one of thirteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT ***599342-76-4*** ***599343-13-2*** ***599343-17-6***
599343-33-6

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses) (amino acid sequence; expressed sequence tags from cDNA libraries derived from human mRNAs having intact 5' ends and their encoded secreted proteins)

RN 599342-76-4 HCAPLUS

CN Protein (human clone CA2343602-SEQID-15273 N-terminal fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 599343-13-2 HCAPLUS

CN Protein (human clone CA2343602-SEQID-15311 N-terminal fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 599343-17-6 HCAPLUS

CN Protein (human clone CA2343602-SEQID-15315 N-terminal fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 599343-33-6 HCAPLUS

CN Protein (human clone CA2343602-SEQID-15331 N-terminal fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 7 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:590711 HCAPLUS

DOCUMENT NUMBER: 139:129339

TITLE: Fluorophore-labeled peptides and FRET assays for clostridial toxins

INVENTOR(S): Steward, Lance E.; Fernandez-Salas, Ester; Aoki, Kei Roger

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 69 pp.

CODEN: USXXCO

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003143651	A1	20030731	US 2001-942098	20010828 <--
WO 2004031773	A1	20040415	WO 2002-US27212	20020822
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
EP 1438586	A1	20040721	EP 2002-807745	20020822
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK				
PRIORITY APPLN. INFO.:			US 2001-942098	A 20010828
			WO 2002-US27212	W 20020822
AB	The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin, including botulinum toxins of all serotypes as well as tetanus toxins. A clostridial toxin substrate of the invention contains a donor fluorophore; an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore; and a clostridial toxin recognition sequence that includes a cleavage site, where the cleavage site intervenes between the donor fluorophore and the acceptor and where, under the appropriate conditions, resonance energy transfer is exhibited between the donor fluorophore and the acceptor.			
IT	***566212-55-3*** ***566212-60-0***			
	RL: PRP (Properties) (unclaimed protein sequence; fluorophore-labeled peptides and FRET assays for clostridial toxins)			
RN	566212-55-3 HCAPLUS			
CN	3: PN: US20030143651 SEQID: 2 unclaimed protein (9CI) (CA INDEX NAME)			
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***				
RN	566212-60-0 HCAPLUS			
CN	26: PN: US20030143651 SEQID: 16 unclaimed protein (9CI) (CA INDEX NAME)			
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***				

L11 ANSWER 8 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:448582 HCAPLUS

Correction of: 2003:154555

DOCUMENT NUMBER: 139:18397

Correction of: 138:182130

TITLE: Differentially expressed nucleic acids and their encoded proteins associated with pain and their use in screening for regulatory agents

INVENTOR(S): Woolf, Clifford; D'Urso, Donatella; Befort, Katia; Costigan, Michael

PATENT ASSIGNEE(S): The General Hospital Corporation, USA; Bayer AG

SOURCE: PCT Int. Appl., 1017 pp.

CODEN: PIXXD2

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003016475	A2	20030227	WO 2002-US25765	20020814 <--
WO 2003016475	A3	20040910		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2003016475	A2	20030227	WO 2002-XA25765	20020814 <--
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2003016475	A2	20030227	WO 2002-XB25765	20020814 <--
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2003016475	A2	20030227	WO 2002-XC25765	20020814 <--
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, MD, RU, TJ, TM			

CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM,
 HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
 LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL,
 PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA,
 UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
 CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
 PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
 NE, SN, TD, TG

WO 2003016475 A2 20030227 WO 2002-XD25765 20020814 <--

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
 CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM,
 HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
 LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL,
 PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA,
 UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
 CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
 PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
 NE, SN, TD, TG

WO 2003016475 A2 20030227 WO 2002-XE25765 20020814 <--

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
 CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM,
 HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
 LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL,
 PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA,
 UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
 CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
 PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
 NE, SN, TD, TG

WO 2003016475 A2 20030227 WO 2002-XF25765 20020814 <--

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
 CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM,
 HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
 LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL,
 PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA,
 UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
 CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
 PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
 NE, SN, TD, TG

EP 1478772 A2 20041124 EP 2002-759358 20020814

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK

PRIORITY APPLN. INFO.:

US 2001-312147P P 20010814
 US 2001-346382P P 20011101
 US 2001-333347P P 20011126
 WO 2002-US25765 A 20020814

AB The present invention relates to human and rat nucleic acid sequences which are related to pain and which are differentially expressed during pain. The nucleic acids are differentially expressed by at least +-1.4-fold in any or all of the following conditions using the Affymetrix human U95, murine U74 and rat U34 GeneChip arrays: axotomy, spared nerve injury, chronic constriction, spinal segmental nerve lesion, and inflammatory pain models. The invention further relates to methods of identifying nucleic acid sequences which are differentially expressed

during pain, microarrays comprising such differentially expressed sequences, and methods of screening agents for the ability to regulate the expression of such differentially expressed sequences. [This abstr. record is one of seven records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT ***537059-16-8***

RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; differentially expressed nucleic acids and their encoded proteins assocd. with pain and their use in screening for regulatory agents)

RN 537059-16-8 HCAPLUS

CN Pain-regulated protein (rat clone WO03016475-SEQID-75) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 9 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:202825 HCAPLUS

DOCUMENT NUMBER: 138:233337

TITLE: FRET protease assays for botulinum serotype A/E toxins

INVENTOR(S): Steward, Lance E.; Fernandez-Salas, Ester; Aoki, Kei
Roger

PATENT ASSIGNEE(S): Allergan, Inc., USA

SOURCE: PCT Int. Appl., 168 pp.

CODEN: PIXXD2

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003020948	A2	20030313	WO 2002-US27145	20020822 <--
WO 2003020948	A3	20030605		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003143650	A1	20030731	US 2001-942024	20010828 <--

PRIORITY APPLN. INFO.:

US 2001-942024 A 20010828

AB The present invention provides clostridial toxin substrates useful in assaying for the protease activity of botulinum serotype A/E toxins. A clostridial toxin substrate of the invention contains a donor fluorophore; an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore; and a clostridial toxin recognition sequence that includes a cleavage site, where the cleavage site intervenes between the donor fluorophore and the acceptor and where, under the appropriate conditions, resonance energy transfer is exhibited between the

donor fluorophore and the acceptor.

IT ***501505-70-0*** ***501505-75-5***

RL: PRP (Properties)
 (unclaimed protein sequence; fRET protease assays for botulinum
 serotype A/E toxins)

RN 501505-70-0 HCAPLUS

CN 2: PN: WO03020948 SEQID: 2 unclaimed protein (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 501505-75-5 HCAPLUS

CN 16: PN: WO03020948 SEQID: 16 unclaimed protein (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 10 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:130959 HCAPLUS

DOCUMENT NUMBER: 138:199734

TITLE: A Drosophila full-length cDNA resource

AUTHOR(S): Stapleton, Mark; Carlson, Joe; Brokstein, Peter; Yu,
 Charles; Champe, Mark; George, Reed; Guarin, Hannibal;
 Kronmiller, Brent; Pacleb, Joanne; Park, Soo; Wan,
 Ken; Rubin, Gerald M.; Celniker, Susan E.

CORPORATE SOURCE: Berkeley Drosophila Genome Project, Lawrence Berkeley
 National Lab., Berkeley, CA, 94720, USA

SOURCE: GenomeBiology (2002), 3(12), No pp. given
 CODEN: GNBLFW; ISSN: 1465-6914
 URL: <http://genomebiology.com/content/pdf/gb-2002-3-12-research0080.pdf>

PUBLISHER: BioMed Central Ltd.

DOCUMENT TYPE: Journal; (online computer file)

LANGUAGE: English

AB A collection of sequenced full-length cDNAs is an important resource both
 for functional genomics studies and for the detn. of the intron-exon
 structure of genes. Providing this resource to the Drosophila
 melanogaster research community has been a long-term goal of the Berkeley
 Drosophila Genome Project. The Drosophila Gene Collection (DGC) has been
 previously described , a set of putative full-length cDNAs that was
 produced by generating and analyzing >250,000 expressed sequence tags
 (ESTs) derived from a variety of tissues and developmental stages.
 High-quality full-insert sequence were generated for 8921 clones in the
 DGC. The sequences of these clones were compared to the annotated Release
 3 genomic sequence, and >5300 cDNAs identified that contain a complete and
 accurate protein-coding sequence. This corresponds to at least one splice
 form for 40% of the predicted D. melanogaster genes. Potential new cases
 of RNA editing were also identified. Thus, comparison of cDNA sequences
 to a high-quality annotated genomic sequence is an effective approach to
 identifying and eliminating defective clones from a cDNA collection.
 Clones were eliminated either because they carry single nucleotide
 discrepancies, which most probably result from reverse transcriptase
 errors, or because they are truncated and contain only part of the
 protein-coding sequence. [This abstr. record is one of five records for
 this document necessitated by the large no. of index entries required to
 fully index the document and publication system constraints.].

IT ***481980-36-3***

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; full-length cDNA sequence resource for Drosophila

melanogaster)
RN 481980-36-3 HCAPLUS
CN RE03722p (Drosophila melanogaster strain y; cn bw sp) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 11 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:84066 HCAPLUS
DOCUMENT NUMBER: 138:199732
TITLE: A Drosophila full-length cDNA resource
AUTHOR(S): Stapleton, Mark; Carlson, Joe; Brokstein, Peter; Yu, Charles; Champe, Mark; George, Reed; Guarin, Hannibal; Kronmiller, Brent; Pacleb, Joanne; Park, Soo; Wan, Ken; Rubin, Gerald M.; Celniker, Susan E.
CORPORATE SOURCE: Berkeley Drosophila Genome Project, Lawrence Berkeley National Lab., Berkeley, CA, 94720, USA
SOURCE: GenomeBiology (2002), 3(12), No pp. given
CODEN: GNBLEW; ISSN: 1465-6914
URL: <http://genomebiology.com/content/pdf/gb-2002-3-12-research0080.pdf>
PUBLISHER: BioMed Central Ltd.
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English

AB A collection of sequenced full-length cDNAs is an important resource both for functional genomics studies and for the detn. of the intron-exon structure of genes. Providing this resource to the Drosophila melanogaster research community has been a long-term goal of the Berkeley Drosophila Genome Project. The Drosophila Gene Collection (DGC) has been previously described , a set of putative full-length cDNAs that was produced by generating and analyzing >250,000 expressed sequence tags (ESTs) derived from a variety of tissues and developmental stages. High-quality full-insert sequence were generated for 8921 clones in the DGC. The sequences of these clones were compared to the annotated Release 3 genomic sequence, and >5300 cDNAs identified that contain a complete and accurate protein-coding sequence. This corresponds to at least one splice form for 40% of the predicted D. melanogaster genes. Potential new cases of RNA editing were also identified. Thus, comparison of cDNA sequences to a high-quality annotated genomic sequence is an effective approach to identifying and eliminating defective clones from a cDNA collection. Clones were eliminated either because they carry single nucleotide discrepancies, which most probably result from reverse transcriptase errors, or because they are truncated and contain only part of the protein-coding sequence. [This abstr. record is one of five records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT ***481817-45-2***

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; full-length cDNA sequence resource for Drosophila melanogaster)

RN 481817-45-2 HCAPLUS
CN LD38682p (Drosophila melanogaster strain y; cn bw sp gene CG3221) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 12 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:55947 HCAPLUS

DOCUMENT NUMBER: 138:84321

TITLE: Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

AUTHOR(S): Strausberg, Robert L.; Feingold, Elise A.; Grouse, Lynette H.; Derge, Jeffery G.; Klausner, Richard D.; Collins, Francis S.; Wagner, Lukas; Shenmen, Carolyn M.; Schuler, Gregory D.; Altschul, Stephen F.; Zeeberg, Barry; Buetow, Kenneth H.; Schaefer, Carl F.; Bhat, Narayan K.; Hopkins, Ralph F.; Jordan, Heather; Moore, Troy; Max, Steve I.; Wang, Jun; Hsieh, Florence; Diatchenko, Luda; Marusina, Kate; Farmer, Andrew A.; Rubin, Gerald M.; Hong, Ling; Stapleton, Mark; Soares, M. Bento; Bonaldo, Maria F.; Casavant, Tom L.; Scheetz, Todd E.; Brownstein, Michael J.; Usdin, Ted B.; Toshiyuki, Shiraki; Carninci, Piero; Prange, Christa; Raha, Sam S.; Loquellano, Naomi A.; Peters, Garrick J.; Abramson, Rick D.; Mullahy, Sara J.; Bosak, Stephanie A.; McEwan, Paul J.; McKernan, Kevin J.; Malek, Joel A.; Gunaratne, Preethi H.; Richards, Stephen; Worley, Kim C.; Hale, Sarah; Garcia, Angela M.; Gay, Laura J.; Hulyk, Stephen W.; Villalon, Debbie K.; Muzny, Donna M.; Sodergren, Erica J.; Lu, Xiuhua; Gibbs, Richard A.; Fahey, Jessica; Helton, Erin; Kettelman, Mark; Madan, Anuradha; Rodrigues, Stephanie; Sanchez, Amy; Whiting, Michelle; Madan, Anup; Young, Alice C.; Shevchenko, Yuriy; Bouffard, Gerard G.; Blakesley, Robert W.; Touchman, Jeffrey W.; Green, Eric D.; Dickson, Mark C.; Rodriguez, Alex C.; Grimwood, Jane; Schmutz, Jeremy; Myers, Richard M.; Butterfield, Yaron S. N.; Krzywinski, Martin I.; Skalska, Ursula; Smailus, Duane E.; Schnerch, Angelique; Schein, Jacqueline E.; Jones, Steven J. M.; Marra, Marco A.

CORPORATE SOURCE: Mammalian Gene Collection (MGC) Program Team, National Cancer Institute, NIH, Bethesda, MD, 20892-2580, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2002), 99(26), 16899-16903
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The National Institutes of Health Mammalian Gene Collection (MGC) Program is a multiinstitutional effort to identify and sequence a cDNA clone contg. a complete ORF for each human and mouse gene. ESTs were generated from libraries enriched for full-length cDNAs and analyzed to identify candidate full-ORF clones, which then were sequenced to high accuracy. The MGC has currently sequenced and verified the full ORF for a nonredundant set of >9000 human and >6000 mouse genes. Candidate full-ORF clones for an addnl. 7800 human and 3500 mouse genes also have been identified. All MGC sequences and clones are available without restriction through public databases and clone distribution networks. [This abstr. record is one of eleven records for this document necessitated by the large no. of index entries required to fully index the

document and publication system constraints.].
IT ***483237-85-0***
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; generation and initial anal. of more than 15,000
full-length human and mouse cDNA sequences)
RN 483237-85-0 HCAPLUS
CN Synaptosomal-associated protein, 25kD (mouse clone MGC:25380
IMAGE:4504644) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 13 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:55564 HCAPLUS

DOCUMENT NUMBER: 138:84319

TITLE: Generation and initial analysis of more than 15,000
full-length human and mouse cDNA sequences

AUTHOR(S): Strausberg, Robert L.; Feingold, Elise A.; Grouse,
Lynette H.; Derge, Jeffery G.; Klausner, Richard D.;
Collins, Francis S.; Wagner, Lukas; Shenmen, Carolyn
M.; Schuler, Gregory D.; Altschul, Stephen F.;
Zeeberg, Barry; Buetow, Kenneth H.; Schaefer, Carl F.;
Bhat, Narayan K.; Hopkins, Ralph F.; Jordan, Heather;
Moore, Troy; Max, Steve I.; Wang, Jun; Hsieh,
Florence; Diatchenko, Luda; Marusina, Kate; Farmer,
Andrew A.; Rubin, Gerald M.; Hong, Ling; Stapleton,
Mark; Soares, M. Bento; Bonaldo, Maria F.; Casavant,
Tom L.; Scheetz, Todd E.; Brownstein, Michael J.;
Usdin, Ted B.; Toshiyuki, Shiraki; Carninci, Piero;
Prange, Christa; Raha, Sam S.; Loquellano, Naomi A.;
Peters, Garrick J.; Abramson, Rick D.; Mullahy, Sara
J.; Bosak, Stephanie A.; McEwan, Paul J.; McKernan,
Kevin J.; Malek, Joel A.; Gunaratne, Preethi H.;
Richards, Stephen; Worley, Kim C.; Hale, Sarah;
Garcia, Angela M.; Gay, Laura J.; Hulyk, Stephen W.;
Villalon, Debbie K.; Muzny, Donna M.; Sodergren, Erica
J.; Lu, Xiuhua; Gibbs, Richard A.; Fahey, Jessica;
Helton, Erin; Kettelman, Mark; Madan, Anuradha;
Rodrigues, Stephanie; Sanchez, Amy; Whiting, Michelle;
Madan, Anup; Young, Alice C.; Shevchenko, Yuriy;
Bouffard, Gerard G.; Blakesley, Robert W.; Touchman,
Jeffrey W.; Green, Eric D.; Dickson, Mark C.;
Rodriguez, Alex C.; Grimwood, Jane; Schmutz, Jeremy;
Myers, Richard M.; Butterfield, Yaron S. N.;
Krzywinski, Martin I.; Skalska, Ursula; Smailus, Duane
E.; Schnerch, Angelique; Schein, Jacqueline E.; Jones,
Steven J. M.; Marra, Marco A.

CORPORATE SOURCE: Mammalian Gene Collection (MGC) Program Team, National
Cancer Institute, NIH, Bethesda, MD, 20892-2580, USA
SOURCE: Proceedings of the National Academy of Sciences of the
United States of America (2002), 99(26), 16899-16903
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The National Institutes of Health Mammalian Gene Collection (MGC) Program
is a multiinstitutional effort to identify and sequence a cDNA clone

contg. a complete ORF for each human and mouse gene. ESTs were generated from libraries enriched for full-length cDNAs and analyzed to identify candidate full-ORF clones, which then were sequenced to high accuracy. The MGC has currently sequenced and verified the full ORF for a nonredundant set of >9000 human and >6000 mouse genes. Candidate full-ORF clones for an addnl. 7800 human and 3500 mouse genes also have been identified. All MGC sequences and clones are available without restriction through public databases and clone distribution networks. [This abstr. record is one of eleven records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT ***480785-03-3*** , GenBank AAH10647
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (amino acid sequence; generation and initial anal. of more than 15,000
 full-length human and mouse cDNA sequences)
 RN 480785-03-3 HCAPLUS
 CN Synaptosomal-associated protein 25, isoform SNAP25A (human clone MGC:9197
 IMAGE:3867544) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 14 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:8418 HCAPLUS

DOCUMENT NUMBER: 138:164527

TITLE: Analysis of the mouse transcriptome based on
 functional annotation of 60,770 full-length cDNAs
 AUTHOR(S): Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.;
 Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito,
 R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.;
 Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.;
 Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.;
 Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin,
 A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J.
 A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L.
 E.; Cousins, S.; Dalla, E.; Dragani, T. A.; Fletcher,
 C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.;
 Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.;
 Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson,
 I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasaki,
 Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.;
 Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.;
 Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie,
 L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.;
 Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.;
 Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.;
 Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring,
 B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.;
 Semple, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.;
 Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita,
 M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.;
 Watanabe, Y.; Wells, C.; Wilming, L. G.;
 Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.;
 Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci,
 P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.;
 Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.;
 Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda,

S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.

CORPORATE SOURCE: Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

SOURCE: Nature (London, United Kingdom) (2002), 420(6915), 563-573

CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs. The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstr. record is one of thirty records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT ***493629-08-6***

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

RN 493629-08-6 HCAPLUS

CN Protein (mouse strain C57BL/6J clone 6330400C21 206-amino acid) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 15 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2002:781494 HCAPLUS

DOCUMENT NUMBER: 138:12031

TITLE: Essential genes in microorganisms and their use as targets for antisense inhibition of proliferation and antibiotic screening

INVENTOR(S): Wang, Liangus; Zamudio, Carlos; Malone, Cheryl; Haselbeck, Robert; Ohlsen, Kari L.; Zyskind, Judith W.; Wall, Daniel; Trawick, John D.; Carr, Grant J.; Yamamoto, Robert; Forsyth, R. Allyn; Xu, H. Howard

PATENT ASSIGNEE(S): Elitra Pharmaceuticals, Inc., USA
 SOURCE: PCT Int. Appl., 1766 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: ***Patent***
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 22
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002077183	A2	20021003	WO 2002-XQ9107	20020321 <--
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, EE, ES, FI, FI, GB, GD, GE, GH, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2002061569	A1	20020523	US 2001-815242	20010321 <--
WO 2002077183	A2	20021003	WO 2002-US9107	20020321 <--
W:	AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
PRIORITY APPLN. INFO.:			US 2001-815242	A 20010321
			US 2001-948993	A 20010906
			US 2001-342923P	P 20011025
			US 2002-72851	A 20020208
			US 2002-362699P	P 20020306
			WO 2002-US9107	A 20020321
			US 2000-191078P	P 20000321
			US 2000-206848P	P 20000523
			US 2000-207727P	P 20000526
			US 2000-242578P	P 20001023
			US 2000-253625P	P 20001127
			US 2000-257931P	P 20001222
			US 2001-269308P	P 20010216

AB The sequences of antisense nucleic acids which inhibit the proliferation of prokaryotes are disclosed. Thus, 6213 nucleic acid fragments are identified for which expression inhibits proliferation or is required for proliferation in *Enterococcus faecalis*, *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, and *Staphylococcus aureus*. Cell-based assays which employ the antisense nucleic acids to identify and develop antibiotics are also disclosed. The antisense nucleic acids can also be used to identify proteins required for proliferation, express these proteins or portions thereof, obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate mols. for rational drug discovery programs. The nucleic acids can also be used to

screen for homologous nucleic acids that are required for proliferation in cells other than Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, and Pseudomonas aeruginosa. The invention provides 38,184 such proliferation-required gene sequences (plus their encoded protein sequences). The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms. [This abstr. record is one of twenty records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT ***477409-05-5***

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(amino acid sequence; essential genes in microorganisms and their use as targets for antisense inhibition of proliferation and antibiotic screening)

RN 477409-05-5 HCAPLUS

CN Protein (Staphylococcus haemolyticus clone SHA100443 essential) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 16 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2002:173232 HCAPLUS

DOCUMENT NUMBER: 136:396926

TITLE: Reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes

INVENTOR(S): Venter, J. Craig; Adams, Mark; Li, Peter W. D.; Myers, Eugene W.

PATENT ASSIGNEE(S): PE Corporation (NY), USA

SOURCE: PCT Int. Appl., 21 pp.

CODEN: PIXXD2

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 10

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001071042	A2	20010927	WO 2001-XA9231	20010323 <--
W:				
AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW:				
GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001071042	A2	20010927	WO 2001-US9231	20010323 <--
WO 2001071042	A3	20030313		
W:				
AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,				

YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-191637P P 20000323
US 2000-614150 A 20000711
WO 2001-US9231 A 20010323

AB The present invention is based on the sequencing and assembly of the *Drosophila melanogaster* genome. The present invention provides the primary nucleotide sequence of a large portion of the *Drosophila melanogaster* genome in a series of genomic and predicted transcript sequences. This information is provided in the form of genomic, transcript and protein sequence information and can be used to generate nucleic acid detection reagents and kits such as nucleic acid arrays. Primary sequences are provided as contiguous strings in a computer-readable format and recorded on media such as floppy disks, hard disks, magnetic tape, CD-ROM, RAM, ROM and hybrids of these categories. Genes/exons can be predicted, sequences can be edited and homol. searches of target motifs can be conducted. [This abstr. record is one of ten records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT ***431198-41-3***

RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; reagents and kits, such as nucleic acid arrays, for detecting expression of over 10,000 *Drosophila* genes)

RN 431198-41-3 HCAPLUS

CN Protein (*Drosophila melanogaster* clone W00171042-SEQID-5994) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 17 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:634532 HCAPLUS

DOCUMENT NUMBER: 136:242628

TITLE: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* pSymA megaplasmid

AUTHOR(S): Barnett, Melanie J.; Fisher, Robert F.; Jones, Ted; Komp, Caridad; Abola, A. Pia; Barloy-Hubler, Frederique; Bowser, Leah; Capela, Delphine; Galibert, Francis; Gouzy, Jerome; Gurjal, Mani; Hong, Andrea; Huizar, Lucas; Hyman, Richard W.; Kahn, Daniel; Kahn, Michael L.; Kalman, Sue; Keating, David H.; Palm, Curtis; Peck, Melicent C.; Surzycki, Raymond; Wells, Derek H.; Yeh, Kuo-Chen; Davis, Ronald W.; Federspiel, Nancy A.; Long, Sharon R.

CORPORATE SOURCE: Department of Biological Sciences, Stanford University, Stanford, CA, 94305, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(17), 9883-9888
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The symbiotic nitrogen-fixing soil bacterium *Sinorhizobium meliloti* contains three replicons: pSymA, pSymB, and the chromosome. We report

here the complete 1354,226-nt sequence of pSymA. In addn. to a large fraction of the genes known to be specifically involved in symbiosis, pSymA contains genes likely to be involved in nitrogen and carbon metab., transport, stress, and resistance responses, and other functions that give *S. meliloti* an advantage in its specialized niche.

IT ***353843-30-8***

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; nucleotide sequence and predicted functions of entire *Sinorhizobium meliloti* pSymA megaplasmid)

RN 353843-30-8 HCAPLUS

CN Protein (*Sinorhizobium meliloti* strain 1021 gene SMa2009) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 18 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:618207 HCAPLUS

DOCUMENT NUMBER: 135:190398

TITLE: Nucleic acid markers useful for the identification, assessment, prevention and therapy of human cancers
INVENTOR(S): Roth, Frederick P.; Van Huffel, Christophe; White, James V.; Shyjan, Andrew W.

PATENT ASSIGNEE(S): Millennium Predictive Medicine, Inc., USA

SOURCE: PCT Int. Appl., 126 pp.

CODEN: PIXXD2

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001061048	A2	20010823	WO 2001-US5263	20010216 <--
WO 2001061048	A3	20030123		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
US 2002051978	A1	20020502	US 2001-788100	20010216 <--

PRIORITY APPLN. INFO.:

US 2000-183312P P 20000217

AB The present invention is directed to the identification of markers that can be used to det. the sensitivity of cancer cells to a therapeutic agent. The present invention is also directed to the identification of therapeutic targets. Nucleic acid arrays were used to det. the level of expression of sequences (genes) found in 60 different solid tumor cancer cell lines selected from the NCI 60 cancer cell line series. Expression anal. was used to identify markers assocd. with sensitivity to certain chemotherapeutic agents.

IT ***126880-89-5*** , Protein SNAP 25 (mouse clone p8.52/p8.51

synaptosome-associated reduced) ***154768-88-4***
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study,
unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical
study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; nucleic acid markers useful for the
identification, assessment, prevention and therapy of human cancers)

RN 126880-89-5 HCAPLUS

CN Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced)
(9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 154768-88-4 HCAPLUS

CN Protein SNAP 25 (human synaptosome-associated isoform a reduced) (9CI)
(CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 19 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:566348 HCAPLUS

DOCUMENT NUMBER: 135:176294

TITLE: The composite genome of the legume symbiont
Sinorhizobium meliloti

AUTHOR(S): Galibert, Francis; Finan, Turlough M.; Long, Sharon
R.; Puhler, Alfred; Abola, Pia; Ampe, Frederic;
Barloy-Hubler, Fredherique; Barnett, Melanie J.;
Becker, Anke; Boistard, Pierre; Bothe, Gordana;
Boutry, Marc; Bowser, Leah; Buhrmester, Jens; Cadieu,
Edouard; Capela, Detphine; Chain, Patrick; Cowie,
Alison; Davis, Ronald W.; Dreanot, Stiphane;
Federspiel, Nancy A.; Fisher, Robert F.; Gloux,
Stephanie; Godrie, Therese; Goffeau, Andre; Golding,
Brian; Gouzy, Jerome; Gurjal, Mani; Hernandez-Lucas,
Ismael; Hong, Andrea; Huizar, Lucas; Hyman, Richard
W.; Jones, Ted; Kahn, Daniel; Kahn, Michael L.;
Kalman, Sue; Keating, David H.; Kiss, Erno; Komp,
Caridad; LeLaure, Valerie; Masuy, David; Palm, Curtis;
Peck, Melicent C.; Pohl, Thomas M.; Portetelle,
Daniel; Purnelle, Benedicte; Ramsperger, Uwe;
Surzycki, Raymond; Thebault, Patricia; Vandenbol,
Micheline; Vorholter, Frank-J.; Weidner, Stefan;
Wells, Derek H.; Wong, Kim; Yeh, Kuo-Chen; Batut,
Jacques

CORPORATE SOURCE: Laboratoire de Genetique et Developpement, Faculte de
Medecine, UMR6061-CNRS, Rennes, F-35043, Fr.

SOURCE: Science (Washington, DC, United States) (2001),
293(5530), 668-672

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The scarcity of usable nitrogen frequently limits plant growth. A tight
metabolic assocn. with rhizobial bacteria allows legumes to obtain
nitrogen compds. by bacterial redn. of dinitrogen (N₂) to ammonium (NH₄⁺).
The annotated DNA sequence of the α -proteobacterium Sinorhizobium
meliloti, the symbiont of alfalfa, is presented. The tripartite
6.7-megabase (Mb) genome comprises a 3.65-Mb chromosome, and 1.35-Mb pSymA
and 1.68-Mb pSymB megaplasmids. Genome sequence anal. indicates that all

three elements contribute, in varying degrees, to symbiosis and reveals how this genome may have emerged during evolution. The genome sequence will be useful in understanding the dynamics of interkingdom assocns. and of life in soil environments. The chromosome, pSymA, and pSymB sequences are available in GenBank Accession Nos. AE007195-AE007315, AL591782-AL591793, and AL603642-AL603647, resp.

IT ***353843-30-8***

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; composite genome of the legume symbiont Sinorhizobium meliloti)

RN 353843-30-8 HCAPLUS

CN Protein (Sinorhizobium meliloti strain 1021 gene SMA2009) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 20 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:444843 HCAPLUS

DOCUMENT NUMBER: 135:41840

TITLE: Expressed sequence tags and encoded human proteins

INVENTOR(S): Dumas, Milne Edwards Jean-Baptiste; Jobert, Severin; Giordano, Jean-Yves

PATENT ASSIGNEE(S): Genset, Fr.

SOURCE: Eur. Pat. Appl., 94 pp.

CODEN: EPXXDW

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 4

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1104808	A1	20010606	EP 2000-202699	20000727 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2311201	AA	20010205	CA 2000-2311201	20000719 <--
US 6639063	B1	20031028	US 2000-621976	20000721 <--
JP 2002010789	A2	20020115	JP 2000-280989	20000807 <--
PRIORITY APPLN. INFO.:			US 1999-147499P	P 19990805

AB The sequences of 5' ESTs and consensus contigated 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs and consensus contigated 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs and consensus contigated 5' ESTs The 5' ESTs and consensus contigated 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs and consensus contigated 5' ESTs. The 5' ESTs and consensus contigated 5' ESTs may also be used to design expression vectors and secretion vectors. [This abstr. record is the second of four records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT ***344403-54-9P***

RL: ANT (Analyte); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); ANST

(Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)

(amino acid sequence; expressed sequence tags and encoded human proteins)

RN 344403-54-9 HCAPLUS

CN Protein (human clone EP1104808-SEQID-7614) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 21 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:185784 HCAPLUS

DOCUMENT NUMBER: 134:232968

TITLE: Protease-resistant SNARE mutants and the uses thereof in rescue of cellular exocytosis for clostridial neurotoxin-poisoned patients

INVENTOR(S): Dolly, James Oliver; O'Sullivan, Gregory A.; Mohammed, Nadiem; Foran, Patrick G.

PATENT ASSIGNEE(S): Imperial College Innovations Limited, UK

SOURCE: PCT Int. Appl., 131 pp.

CODEN: PIXXD2

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001018038	A2	20010315	WO 2000-GB3196	20000818 <--
WO 2001018038	A3	20011011		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
CA 2379532	AA	20010315	CA 2000-2379532	20000818 <--
EP 1210444	A2	20020605	EP 2000-956652	20000818 <--
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL			
JP 2003508092	T2	20030304	JP 2001-522260	20000818 <--
PRIORITY APPLN. INFO.:			US 1999-149993P	P 19990820
			WO 2000-GB3196	W 20000818

AB A method of treating a patient suffering from poisoning by clostridial toxin wherein a SNARE (sol. (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) that is resistant to proteolysis by the said clostridial toxin (toxin-resistant SNARE) and/or is capable of inhibiting the clostridial toxin is supplied to a cell of the patient. The SNARE that is resistant to proteolysis may be, synaptosomal-assocd. polypeptide of 25 kDA (SNAP-25). The SNAP-25 is preferably resistant to proteolysis by BoNT/A, BoNT/E and BoNT/C. A method of treating a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis wherein a deriv. (inhibitory SNARE) that is capable of inhibiting SNARE-dependent exocytosis is supplied to the said cell of the patient. The inhibitory SNARE may be a fragment of

SNAP-25 that is derivable by cleavage of SNAP-25 by botulinum toxin A (BoNT/A). The cell may be, for example, a nerve cell, adreno-chromaffin cell or insulin-secreting cell. The SNARE may be supplied to the cell by expressing recombinant polynucleotide construct. The SNARE or construct may be targeted to a nerve cell, by means of an inactive clostridial neurotoxin. The SNARE may be expressed under the target cell-specific promoter.

IT ***126880-89-5*** , Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced) ***154768-88-4*** ***329758-74-9***
 RL: PRP (Properties)
 (unclaimed protein sequence; protease-resistant SNARE mutants and the uses thereof in rescue of cellular exocytosis for clostridial neurotoxin-poisoned patients)
 RN 126880-89-5 HCAPLUS
 CN Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 154768-88-4 HCAPLUS
 CN Protein SNAP 25 (human synaptosome-associated isoform a reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 329758-74-9 HCAPLUS
 CN 38: PN: WO0118038 FIGURE: 8 unclaimed protein (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 22 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 2001:7597 HCAPLUS
 DOCUMENT NUMBER: 134:91082
 TITLE: Peptide inhibitors of neurotransmitter secretion by neuronal cells
 INVENTOR(S): Montal, Mauricio; Canaves, Jaume M.; Ferrer-Monteil, Antonio V.
 PATENT ASSIGNEE(S): The Regents of the University of California, USA
 SOURCE: U.S., 23 pp.
 CODEN: USXXAM
 DOCUMENT TYPE: ***Patent***
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6169074	B1	20010102	US 1997-819286	19970318 <--
PRIORITY APPLN. INFO.:			US 1996-13599P	P 19960318

AB The invention consists of peptides which inhibit the secretion of neurotransmitters from synaptic vesicles. The peptides of the invention are believed to mimic the activity of neurotoxins produced by Clostridium botulinum and tetani (including botulinum serotypes A, B, C, D, E, F and G). Structurally, the peptides are comprised of amino acid fragments from the substrate binding domains selected from three proteins which bind to form a receptor for docking of synaptic vesicles to the plasma membranes of neuronal cells; i.e., SNAP-25, VAMP-2 and syntaxin. Certain of the inventive peptides exhibit strong inhibitory activity; e.g., 50% or greater decline in neurotransmitter release is obtained at even nanomolar

concns. The peptides are suited for use as substitutes for Clostridium neurotoxins in clin. applications and in compds. for targeted delivery of drugs into neural cells.

IT ***126880-89-5*** , Protein SNAP 25 (mouse clone p8.52/p8.51
synaptosome-associated reduced)
RL: PRP (Properties)
(unclaimed protein sequence; peptide inhibitors of neurotransmitter
secretion by neuronal cells)
RN 126880-89-5 HCAPLUS
CN Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced)
(9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 23 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:710448 HCAPLUS

DOCUMENT NUMBER: 133:262341

TITLE: Expressed sequence tags and encoded human proteins

INVENTOR(S): Dumas Milne Edwards, Jean-Baptiste; Duclert, Aymeric;
Giordano, Jean-Yves

PATENT ASSIGNEE(S): Genset, Fr.

SOURCE: Eur. Pat. Appl., 71 pp.

CODEN: EPXXDW

DOCUMENT TYPE: ***Patent***

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 8

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1033401	A2	20000906	EP 2000-200610	20000221 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1033401	A2	20000906	EP 2000-200610	20000221 <--
EP 1033401	A3	20040421		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.: US 1999-122487P P 19990226
EP 2000-200610 A 20000221

AB The sequences of 5' ESTs derived from human mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors. [This abstr. record is the second of 8 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT ***296817-03-3*** ***297133-02-9***
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; expressed sequence tags and encoded human proteins)
RN 296817-03-3 HCAPLUS

CN Protein (human clone EP1033401_SEQID_7906 fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 297133-02-9 HCAPLUS

CN Protein (human clone EP1033401_SEQID_4845 fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 24 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:230405 HCAPLUS

DOCUMENT NUMBER: 132:304167

TITLE: The genome sequence of Drosophila melanogaster

AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian;

Murphy, Lee; Muzny, Donna M.; Nelson, David L.;
 Nelson, David R.; Nelson, Keith A.; Nixon, Katherine;
 Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo,
 Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John;
 Puri, Vinita; Reese, Martin G.; Reinert, Knut;
 Remington, Karin; Saunders, Robert D. C.; Scheeler,
 Frederick; Shen, Hua; Shue, Bixiang Christopher;
 Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian
 P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.;
 Stapleton, Mark; Strong, Renee; Sun, Eric; Svirska,
 Robert; Tector, Cyndee; Turner, Russell; Venter, Eli;
 Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman,
 David A.; Weinstock, George M.; Weissenbach, Jean;
 Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.;
 Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh,
 Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang,
 Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun
 H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu,
 Shiao ping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs,
 Richard A.; Myers, Eugene W.; Rubin, Gerald M.;
 Venter, J. Craig

CORPORATE SOURCE:

SOURCE:

Celera Genomics, Rockville, MD, 20850, USA

Science (Washington, D. C.) (2000), 287(5461),
 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER:

American Association for the Advancement of Science

DOCUMENT TYPE:

Journal

LANGUAGE:

English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was detd. of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT ***262956-68-3***

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)

(amino acid sequence; genome sequence of *Drosophila melanogaster*)

RN 262956-68-3 HCAPLUS

CN Protein (*Drosophila melanogaster* gene CG3221) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT:

89

THERE ARE 89 CITED REFERENCES AVAILABLE FOR THIS
 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 25 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1998:608637 HCAPLUS
DOCUMENT NUMBER: 129:212540
TITLE: Cloning, sequence, and expression of human and rat
gene Hrs-2 and encoded ATPase for modulation of
vesicular release
INVENTOR(S): Bean, Andrew J.; Scheller, Richard H.
PATENT ASSIGNEE(S): The Board of Trustees of the Leland Stanford Junior
University, USA
SOURCE: PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DOCUMENT TYPE: ***Patent***
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9838210	A2	19980903	WO 1998-US3789	19980226 <--
W: AU, CA, CN, JP, KR				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9864407	A1	19980918	AU 1998-64407	19980226 <--
PRIORITY APPLN. INFO.:			US 1997-39159P	P 19970226
			WO 1998-US3789	W 19980226
AB Rat and human gene Hrs-2 polynucleotides and encoded ATPase polypeptides are disclosed. Also disclosed are methods of identifying a compd. capable of modulating calcium-regulated secretion of secretory vesicles, such as the release of neurotransmitter-contg. synaptic vesicles. Thus, drugs capable of modulating or inhibiting the interaction between the SNAP-25 protein and gene Hrs-2 protein can be detected in a small mol. combinatorial library. Potential identified drugs may be useful in treating central nervous system diseases.				
IT ***126880-89-5*** , Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced) RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process) (amino acid sequence; cloning, sequence, and expression of human and rat gene Hrs-2 and encoded ATPase for modulation of vesicular release)				
RN 126880-89-5 HCAPLUS				
CN Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced) (9CI) (CA INDEX NAME)				

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 26 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1994:264093 HCAPLUS
DOCUMENT NUMBER: 120:264093
TITLE: Human cDNA clones encoding two different isoforms of
the nerve terminal protein SNAP-25
AUTHOR(S): Bark, I. Christina; Wilson, Michael C.
CORPORATE SOURCE: Dep. Neuropharmacol., Scripps Res. Inst., La Jolla,
CA, 92037, USA
SOURCE: Gene (1994), 139(2), 291-2
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two distinct cDNA sequences, corresponding to alternative isoforms of the human nerve terminal protein SNAP-25 (synaptosomal-assocd. protein of 25 kDa), were cloned and characterized. Sequence anal. demonstrated that the 2 isoforms are generated by alternative splicing between 2 distinct but homologous exons 5, a and b, each encoding 39 amino acids (aa). Although the 2 isoforms, SNAP-25a and SNAP-25b, differ by only 9 aa, this domain encodes the portion of the protein that is a substrate for post-translational fatty acetylation, and therefore might be important for regulating subcellular localization and membrane targeting.

IT ***126880-89-5*** , GenBank L19761-derived protein ***154768-88-4***

GenBank L19760-derived protein
RL: PRP (Properties)
(amino acid sequence of, alternatively spliced isoform in relation to)
RN 126880-89-5 HCAPLUS
CN Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 154768-88-4 HCAPLUS
CN Protein SNAP 25 (human synaptosome-associated isoform a reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 27 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STM
ACCESSION NUMBER: 1991:446514 HCAPLUS
DOCUMENT NUMBER: 115:46514
TITLE: Expression of a conserved cell-type-specific protein in nerve terminals coincides with synaptogenesis
AUTHOR(S): Catsicas, Stefano; Larhammar, Dan; Blomqvist, Anders; Sanna, Pietro Paolo; Milner, Robert J.; Wilson, Michael C.
CORPORATE SOURCE: Res. Inst., Scripps Clin., La Jolla, CA, 92037, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1991), 88(3), 785-9
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Contact of axons with target territories results in the formation of synapses, specific junctional complexes that may represent a final stage of neuronal maturation. Synaptosomal-assocd. protein 25 (SNAP-25) is a component of particular nerve terminals recently identified in rodent brain. To evaluate the structure and regulation of mol. components of the synapse, the expression of SNAP-25 was examd. in the developing chicken nervous system. Anal. of SNAP-25 cDNA clones demonstrated that the chicken homolog is identical in amino acid sequence to the mouse protein. In chicken retina and neural tube, the onset of SNAP-25 mRNA and protein expression corresponded to the time of synaptogenesis. Thus, SNAP-25 may play a role in the physiol. of mature nerve terminals, and its expression may be regulated by specific cell-cell interactions occurring during synapse formation.

IT ***126880-89-5*** , Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced)
RL: PRP (Properties)
(amino acid sequence of)
RN 126880-89-5 HCAPLUS

CN Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced)
(9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L11 ANSWER 28 OF 28 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1990:195624 HCAPLUS

DOCUMENT NUMBER: 112:195624

TITLE: The identification of a novel synaptosomal-associated protein, SNAP-25, differentially expressed by neuronal subpopulations

AUTHOR(S): Oyler, George A.; Higgins, Gerald A.; Hart, Richard A.; Battenberg, Elena; Billingsley, Melvin; Bloom, Floyd E.; Wilson, Michael C.

CORPORATE SOURCE: Dep. Mol. Biol., Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA

SOURCE: Journal of Cell Biology (1989), 109(6, Pt. 1), 3039-52
CODEN: JCLBA3; ISSN: 0021-9525

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The cDNA clones of a neuronal-specific mRNA encoding a novel 25-kilodalton (kD) synaptosomal protein, SNAP-25, that is widely but differentially expressed by diverse neuronal subpopulations of the mammalian nervous system were isolated and characterized. The sequence of the SNAP-25 cDNA revealed a single open reading frame that encodes a primary translation product of 206 amino acids. Antisera elicited against a 12-amino acid peptide, corresponding to the C-terminal residues of the predicted polypeptide sequence, recognized a single 25-kD protein that is associated with synaptosomal fractions of hippocampal preps. The SNAP-25 polypeptide remains associated with synaptosomal membrane components after hypoosmotic lysis and is released by nonionic detergent but not high salt extraction. Although the SNAP-25 polypeptide lacks a hydrophobic stretch of residues compatible with a transmembrane region, the N-terminus may form an amphiphilic helix that may facilitate alignment with membranes. The predicted amino acid sequence also includes a cluster of 4 closely spaced cysteine residues, similar to the metal-binding domains of some metalloproteins, suggesting that the SNAP-25 polypeptide may have the potential to coordinately bind metal ions. Consistent with the protein fractionation, light and electron microscopic immunocytochemistry indicated that SNAP-25 is located within the presynaptic terminals of hippocampal mossy fibers and the inner molecular layer of the dentate gyrus. The mRNA was enriched within neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum. The distribution of the SNAP-25 mRNA and the association of the protein with presynaptic elements suggest that SNAP-25 may play an important role in the synaptic function of specific neuronal systems.

IT ***126880-89-5*** , Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced)

RL: PRP (Properties)

(amino acid sequence of)

RN 126880-89-5 HCAPLUS

CN Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced)
(9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

=> select hit rn l1l 1-28
E1 THROUGH E31 ASSIGNED

=> fil reg
FILE 'REGISTRY' ENTERED AT 11:40:20 ON 08 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 7 FEB 2005 HIGHEST RN 827299-31-0
DICTIONARY FILE UPDATES: 7 FEB 2005 HIGHEST RN 827299-31-0

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> => d his l12

(FILE 'HCAPLUS' ENTERED AT 11:34:37 ON 08 FEB 2005)
SELECT HIT RN L1l 1-28

FILE 'REGISTRY' ENTERED AT 11:40:20 ON 08 FEB 2005
L12 31 S E1-E31 AND L1

=>
=>

=> d .seq l12 1-31

L12 ANSWER 1 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***825667-86-5*** REGISTRY
CN INDEX NAME NOT YET ASSIGNED
SQL 206
RN ***825667-86-5*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

L12 ANSWER 2 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***599431-67-1*** REGISTRY
CN Protein (human clone CA2343602-SEQID-24942) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 942: PN: CA2343602 SEQID: 24942 claimed protein
NTE

type	----- location -----	description
uncommon	Aaa-2 - -	
uncommon	Aaa-39 - -	

SQL 51
RN ***599431-67-1*** REGISTRY

SEQ 1 MXEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEEXK SSDAYKKS LG
=====

HITS AT: 12-17

REFERENCE 1: 139:241383

L12 ANSWER 3 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***599373-73-6*** REGISTRY
CN Protein (human clone CA2343602-SEQID-20804) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 804: PN: CA2343602 SEQID: 20804 claimed protein
SQL 68
RN ***599373-73-6*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLV ML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:241382

L12 ANSWER 4 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***599366-06-0*** REGISTRY
CN Protein (human clone CA2343602-SEQID-20246) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 246: PN: CA2343602 SEQID: 20246 claimed protein
NTE

type	----- location -----	description
uncommon	Aaa-68 - -	

SQL 68
RN ***599366-06-0*** REGISTRY

SEQ 1 MAEYADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLV ML
=====

HITS AT: 12-17

REFERENCE 1: 139:241382

L12 ANSWER 5 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***599359-79-2*** REGISTRY
CN Protein (human clone CA2343602-SEQID-17002 N-terminal fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1002: PN: CA2343602 SEQID: 17002 claimed protein
SQL 88

RN ***599359-79-2*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML

=====

HITS AT: 12-17

REFERENCE 1: 139:241381

L12 ANSWER 6 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***599359-78-1*** REGISTRY

CN Protein (human clone CA2343602-SEQID-17001 N-terminal fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1001: PN: CA2343602 SEQID: 17001 claimed protein

SQL 101

RN ***599359-78-1*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML

=====

HITS AT: 12-17

REFERENCE 1: 139:241381

L12 ANSWER 7 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***599343-33-6*** REGISTRY

CN Protein (human clone CA2343602-SEQID-15331 N-terminal fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3329: PN: CA2343602 SEQID: 15331 claimed protein

SQL 126

RN ***599343-33-6*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML

=====

HITS AT: 12-17

REFERENCE 1: 139:241380

L12 ANSWER 8 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***599343-17-6*** REGISTRY

CN Protein (human clone CA2343602-SEQID-15315 N-terminal fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3313: PN: CA2343602 SEQID: 15315 claimed protein

NTE

type	location	description
uncommon	Aaa-72	-

SQL 100

RN ***599343-17-6*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML

=====

HITS AT: 12-17

REFERENCE 1: 139:241380

L12 ANSWER 9 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***599343-13-2*** REGISTRY

CN Protein (human clone CA2343602-SEQID-15311 N-terminal fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3309: PN: CA2343602 SEQID: 15311 claimed protein

SQL 105

RN ***599343-13-2*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML

=====

HITS AT: 12-17

REFERENCE 1: 139:241380

L12 ANSWER 10 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***599342-76-4*** REGISTRY

CN Protein (human clone CA2343602-SEQID-15273 N-terminal fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3271: PN: CA2343602 SEQID: 15273 claimed protein

NTE

type	-----	location	-----	description
uncommon		Aaa-69	-	-
uncommon		Aaa-72	-	-
uncommon		Aaa-73	-	-
uncommon		Aaa-84	-	-
uncommon		Aaa-85	-	-

SQL 105

RN ***599342-76-4*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML

=====

HITS AT: 12-17

REFERENCE 1: 139:241380

L12 ANSWER 11 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***566212-60-0*** REGISTRY

CN 26: PN: US20030143651 SEQID: 16 unclaimed protein (9CI) (CA INDEX NAME)

SQL 249

RN ***566212-60-0*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML

=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:129339

L12 ANSWER 12 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***566212-55-3*** REGISTRY
CN 3: PN: US20030143651 SEQID: 2 unclaimed protein (9CI) (CA INDEX NAME)
SQL 206
RN ***566212-55-3*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:129339

L12 ANSWER 13 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***537059-16-8*** REGISTRY

CN Pain-regulated protein (rat clone WO03016475-SEQID-75) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 75: PN: WO03016475 SEQID: 75 claimed protein

SQL 206

RN ***537059-16-8*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:18397

L12 ANSWER 14 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***501505-75-5*** REGISTRY

CN 16: PN: WO03020948 SEQID: 16 unclaimed protein (9CI) (CA INDEX NAME)

SQL 249

RN ***501505-75-5*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:233337

L12 ANSWER 15 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***501505-70-0*** REGISTRY

CN 2: PN: WO03020948 SEQID: 2 unclaimed protein (9CI) (CA INDEX NAME)

SQL 206

RN ***501505-70-0*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:233337

L12 ANSWER 16 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***493629-08-6*** REGISTRY
CN Protein (mouse strain C57BL/6J clone 6330400C21 206-amino acid) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAC37105
CN GenBank BAC37105 (Translated from: GenBank AK078038)
SQL 206
RN ***493629-08-6*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:164527

L12 ANSWER 17 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***483237-85-0*** REGISTRY
CN Synaptosomal-associated protein, 25kD (mouse clone MGC:25380 IMAGE:4504644) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAH18249
CN GenBank AAH18249 (Translated from: GenBank BC018249)
CN Snap25 protein (mouse clone MGC:25380 IMAGE:4504644)
SQL 206
RN ***483237-85-0*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 142:18189

REFERENCE 2: 138:84321

L12 ANSWER 18 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***481980-36-3*** REGISTRY
CN RE03722p (Drosophila melanogaster strain y; cn bw sp) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAM29386
CN GenBank AAM29386 (Translated from: GenBank AY113381)
SQL 82
RN ***481980-36-3*** REGISTRY

SEQ 51 RRQQQRAEEM QRREEEAARQ GQGQSNLRWQ TS
=== ===

HITS AT: 58-63

REFERENCE 1: 138:199734

L12 ANSWER 19 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***481817-45-2*** REGISTRY
CN LD38682p (Drosophila melanogaster strain y; cn bw sp gene CG3221) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN GenBank AAL13907
CN GenBank AAL13907 (Translated from: GenBank AY058678)

SQL 537

RN ***481817-45-2*** REGISTRY

SEQ 1 MEMFFKFLSG NITDANILTE RQVLEREEMQ RRGWLSASD RELKLLQIEA
=====

HITS AT: 27-32

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:199732

L12 ANSWER 20 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***480785-03-3*** REGISTRY

CN Synaptosomal-associated protein 25, isoform SNAP25A (human clone MGC:9197
IMAGE:3867544) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAH10647
CN GenBank AAH10647 (Translated from: GenBank BC010647)
CN Similar to synaptosomal-associated protein, 25kD (human clone MGC:9197
IMAGE:3867544)

SQL 206

RN ***480785-03-3*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 142:18186

REFERENCE 2: 138:84319

L12 ANSWER 21 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***477409-05-5*** REGISTRY

CN Protein (Staphylococcus haemolyticus clone SHA100443 essential) (9CI) (CA
INDEX NAME)

OTHER NAMES:

CN 1377: PN: WO02077183 SEQID: 71377 claimed protein

SQL 93

RN ***477409-05-5*** REGISTRY

SEQ 1 IKPHATVITL DIQ GKMLSSE GLAEEMQRRM TQGQSDVFV IGGSNGLHED
=====

HITS AT: 24-29

REFERENCE 1: 138:12031

L12 ANSWER 22 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***459518-10-6*** REGISTRY

CN GenBank BAA22370 (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 77: PN: WO2004038376 TABLE: 5 unclaimed protein
CN 969: PN: WO03091391 FIGURE: 20 unclaimed protein
CN GenBank BAA22370 (Translated from: GenBank D21267)
SQL 206
RN ***459518-10-6*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 140:402911

REFERENCE 2: 139:363045

L12 ANSWER 23 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***431198-41-3*** REGISTRY

CN Protein (Drosophila melanogaster clone WO0171042-SEQID-5994) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1989: PN: WO0171042 SEQID: 5994 claimed protein

SQL 537

RN ***431198-41-3*** REGISTRY

SEQ 1 MEMFFKFLSG NITDANILTE RQVLEREEMQ RRGWLSASD RELKLLQIEA
=====

HITS AT: 27-32

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:396926

L12 ANSWER 24 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***353843-30-8*** REGISTRY

CN Protein (Sinorhizobium meliloti strain 1021 gene SMa2009) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAK65758

CN GenBank AAK65758 (Translated from: GenBank AE007296)

SQL 149

RN ***353843-30-8*** REGISTRY

SEQ 101 ALRAAADQGY GERVAMVVDV FGHRWMLSQK IEDVALEEMQ RRWNEQTGA
=====

HITS AT: 137-142

REFERENCE 1: 136:242628

REFERENCE 2: 135:176294

L12 ANSWER 25 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN

RN ***344403-54-9*** REGISTRY

CN Protein (human clone EP1104808-SEQID-7614) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 75: PN: EP1104808 SEQID: 7614 claimed protein

```

SQL 68
RN ***344403-54-9*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====
HITS AT: 12-17

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE 1: 135:41840

L12 ANSWER 26 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***329758-74-9*** REGISTRY
CN 38: PN: WO0118038 FIGURE: 8 unclaimed protein (9CI) (CA INDEX NAME)
SQL 206
RN ***329758-74-9*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====
HITS AT: 12-17

REFERENCE 1: 134:232968

L12 ANSWER 27 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***297133-02-9*** REGISTRY
CN Protein (human clone EP1033401_SEQID_4845 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 311: PN: EP1033401 SEQID: 4845 claimed protein
SQL 64
RN ***297133-02-9*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====
HITS AT: 12-17

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE 1: 133:262341

L12 ANSWER 28 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***296817-03-3*** REGISTRY
CN Protein (human clone EP1033401_SEQID_7906 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1152: PN: EP1033401 SEQID: 7906 claimed protein
NTE
-----
type          ----- location ----- description
-----
uncommon      Aaa-71          -          -
uncommon      Aaa-72          -          -
uncommon      Aaa-92          -          -
-----

SQL 106
RN ***296817-03-3*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

```


HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 133:262341

L12 ANSWER 29 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***262956-68-3*** REGISTRY
CN Protein (Drosophila melanogaster gene CG3221) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAF46650
CN GenBank AAF46650 (Translated from: GenBank AE003452)
SQL 537
RN ***262956-68-3*** REGISTRY

SEQ 1 MEMFFKFLSG NITDANILTE RQVLEREEMQ RRGWLSASD RELKLLQIEA
=====

HITS AT: 27-32

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:304167

L12 ANSWER 30 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***154768-88-4*** REGISTRY
CN Protein SNAP 25 (human synaptosome-associated isoform a reduced) (9CI)
(CA INDEX NAME)
OTHER NAMES:
CN 31: PN: WO0118038 FIGURE: 8 unclaimed protein
CN Protein SNAP 25 (synaptosome-associated protein, 25,000-kilodalton) (human
gene SNAP)
SQL 206
RN ***154768-88-4*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML
=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:190398

REFERENCE 2: 134:232968

REFERENCE 3: 120:264093

L12 ANSWER 31 OF 31 REGISTRY COPYRIGHT 2005 ACS on STN
RN ***126880-89-5*** REGISTRY
CN Protein SNAP 25 (mouse clone p8.52/p8.51 synaptosome-associated reduced)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: US6169074 SEQID: 1 unclaimed protein
CN 33: PN: WO0118038 FIGURE: 8 unclaimed protein
CN Protein (human clone hgb674 gene HUMSNAP25B(F))
CN Protein SNAP 25 (chicken clone 4.1c/4.1d synaptosome-associated reduced)
CN Protein SNAP 25 (human synaptosome-associated isoform b reduced)
CN Protein SNAP-25 (synaptosome-assocd. protein) (mouse)

SQL 206

RN ***126880-89-5*** REGISTRY

SEQ 1 MAEDADMRNE LEEMQRRADQ LADESLESTR RMLQLVEESK DAGIRTLVML

=====

HITS AT: 12-17

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:190398

REFERENCE 2: 134:232968

REFERENCE 3: 134:91082

REFERENCE 4: 129:212540

REFERENCE 5: 120:264093

REFERENCE 6: 115:46514

REFERENCE 7: 112:195624

=>